



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/680,963
Source: IFWO
Date Processed by STIC: 12/21/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/680,963

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not** exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 ✓ Skipped Sequences Sequence(s) 7-8 missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number *← This is the valid format for intentionally skipped sequences.*
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
 Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 12/21/2004

PATENT APPLICATION: US/10/680,963

TIME: 11:33:40

Input Set : A:\GFI-108 Sequence listing.ST25.txt

Output Set: N:\CRF4\12212004\J680963.raw

pp 1-3,6

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: GlycoFi, Inc.
 4 Bobrowicz, Piotr
 5 Hamilton, Stephen R.
 6 Gerngross, Tilman U.
 7 Wildt, Stefan
 8 Choi, Byung-Kwon
 9 Nett, Juergen H.
 10 Davidson, Robert C.
 12 <120> TITLE OF INVENTION: N-Acetylglucosaminyltransferase III expression in lower
 13 eukaryotes
 15 <130> FILE REFERENCE: GFI-108 CIP
 17 <140> CURRENT APPLICATION NUMBER: US 10/680,963
 18 <141> CURRENT FILING DATE: 2003-10-07
 20 <150> PRIOR APPLICATION NUMBER: US 10/371,877
 21 <151> PRIOR FILING DATE: 2003-02-20
 23 <150> PRIOR APPLICATION NUMBER: US 09/892,591
 24 <151> PRIOR FILING DATE: 2001-06-27
 26 <150> PRIOR APPLICATION NUMBER: US 60/214,358
 27 <151> PRIOR FILING DATE: 2000-06-28
 29 <150> PRIOR APPLICATION NUMBER: US 60/215,638
 30 <151> PRIOR FILING DATE: 2000-06-30
 32 <150> PRIOR APPLICATION NUMBER: US 60/279,997
 33 <151> PRIOR FILING DATE: 2001-03-30
 35 <150> PRIOR APPLICATION NUMBER: PCT/US02/41510
 36 <151> PRIOR FILING DATE: 2002-12-24
 38 <150> PRIOR APPLICATION NUMBER: US 60/344,169
 39 <151> PRIOR FILING DATE: 2001-12-27
 41 <160> NUMBER OF SEQ ID NOS: 101
 43 <170> SOFTWARE: PatentIn version 3.2
 45 <210> SEQ ID NO: 1
 46 <211> LENGTH: 3
 47 <212> TYPE: PRT
 48 <213> ORGANISM: artificial
 50 <220> FEATURE:
 51 <223> OTHER INFORMATION: Glycosylation target
 54 <220> FEATURE:
 55 <221> NAME/KEY: MISC_FEATURE
 56 <222> LOCATION: (2)..(2)
 57 <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
 59 <400> SEQUENCE: 1
 W--> 61 Asn Xaa Ser
 62 1
 65 <210> SEQ ID NO: 2

*give source of genetic material
(see item 11 on Enr Summary
Sheet)*

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Input Set : A:\GFI-108 Sequence listing.ST25.txt

Output Set: N:\CRF4\12212004\J680963.raw

```

66 <211> LENGTH: 3
67 <212> TYPE: PRT
68 <213> ORGANISM: artificial
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Glycosylation target same error
74 <220> FEATURE:
75 <221> NAME/KEY: MISC_FEATURE
76 <222> LOCATION: (2)..(2)
77 <223> OTHER INFORMATION: wherein "Xaa" is any amino acid except proline
79 <400> SEQUENCE: 2
W--> 81 Asn Xaa Thr
82 1
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 21
87 <212> TYPE: DNA
88 <213> ORGANISM: artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,6-
mannosyltransferase)
93 <400> SEQUENCE: 3
94 atggcgaagg cagatggcag t 21
97 <210> SEQ ID NO: 4
98 <211> LENGTH: 21
99 <212> TYPE: DNA
100 <213> ORGANISM: artificial
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,6-
mannosyltransferase)
105 <400> SEQUENCE: 4
106 ttagtccttc caacttcctt c 21
109 <210> SEQ ID NO: 5
110 <211> LENGTH: 26
111 <212> TYPE: DNA
112 <213> ORGANISM: artificial
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,2
mannosyltransferases)
116
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (9)..(9)
122 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
124 <220> FEATURE:
125 <221> NAME/KEY: misc_feature
126 <222> LOCATION: (12)..(12)
127 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (18)..(18)
132 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
134 <400> SEQUENCE: 5
W--> 135 taytgmgng tngarcynga yathaa 26

```

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Input Set : A:\GFI-108 Sequence listing.ST25.txt

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138 <210> SEQ ID NO: 6
 139 <211> LENGTH: 20
 140 <212> TYPE: DNA
 141 <213> ORGANISM: artificial
 143 <220> FEATURE:
 144 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,2
 145 mannosyltransferases)
 148 <220> FEATURE:
 149 <221> NAME/KEY: misc_feature
 150 <222> LOCATION: (6)..(6)
 151 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 153 <220> FEATURE:
 154 <221> NAME/KEY: misc_feature
 155 <222> LOCATION: (12)..(12)
 156 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
 158 <400> SEQUENCE: 6

W--> 159 gcrtcncccc anckytcrta

20

162 <210> SEQ ID NO: 7
 163 <211> LENGTH: 0
 164 <212> TYPE: DNA
 165 <213> ORGANISM: Kluyveromyces lactis
 167 <400> SEQUENCE: 7

*delete this section
 (see item 8 on Error summary sheet)
 for valid format*

W--> 168 000

170 <210> SEQ ID NO: 8
 171 <211> LENGTH: 0
 172 <212> TYPE: PRT
 173 <213> ORGANISM: Kluyveromyces lactis
 175 <400> SEQUENCE: 8

delete

*Do the same with
 sequences 43 and 44*

W--> 176 000

178 <210> SEQ ID NO: 9
 179 <211> LENGTH: 458
 180 <212> TYPE: PRT
 181 <213> ORGANISM: Saccharomyces cerevisiae
 184 <220> FEATURE:
 185 <221> NAME/KEY: MISC_FEATURE
 186 <222> LOCATION: (304)..(318)
 187 <223> OTHER INFORMATION: Low-complexity sequence
 189 <220> FEATURE:
 190 <221> NAME/KEY: MISC_FEATURE
 191 <222> LOCATION: (416)..(436)
 192 <223> OTHER INFORMATION: Low-complexity sequence
 194 <400> SEQUENCE: 9

*yes, but which amino acid(s) do
 the Xaa's represent?*

same error

196 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
 197 1 5 10 15
 200 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
 201 20 25 30
 204 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 205 35 40 45
 208 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Lys Lys

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Input Set : A:\GFI-108 Sequence listing.ST25.txt

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```

209      50      55      60
212 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
213 65      70      75      80
216 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
217      85      90      95
220 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
221      100      105      110
224 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
225      115      120      125
228 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
229      130      135      140
232 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
233 145      150      155      160
236 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
237      165      170      175
240 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
241      180      185      190
244 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
245      195      200      205
248 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
249      210      215      220
252 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
253 225      230      235      240
256 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
257      245      250      255
260 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
261      260      265      270
264 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
265      275      280      285
W--> 268 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
269      290      295      300
272 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
273 305      310      315      320
276 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
277      325      330      335
280 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
281      340      345      350
284 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
285      355      360      365
288 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
289      370      375      380
292 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
293 385      390      395      400
296 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa
297      405      410      415
300 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
301      420      425      430
304 Xaa Xaa Xaa Xaa Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
305      435      440      445

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```

308 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
309      450                      455
312 <210> SEQ ID NO: 10
313 <211> LENGTH: 458
314 <212> TYPE: PRT
315 <213> ORGANISM: Saccharomyces cerevisiae
317 <400> SEQUENCE: 10
319 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
320 1      5      10      15
323 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
324      20      25      30
327 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
328      35      40      45
331 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Lys Lys
332      50      55      60
335 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
336 65      70      75      80
339 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
340      85      90      95
343 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
344      100     105     110
347 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
348      115     120     125
351 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
352      130     135     140
355 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
356 145     150     155     160
359 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
360      165     170     175
363 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
364      180     185     190
367 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
368      195     200     205
371 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
372      210     215     220
375 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
376 225     230     235     240
379 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
380      245     250     255
383 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
384      260     265     270
387 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
388      275     280     285
391 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
392      290     295     300
395 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
396 305     310     315     320
399 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
400      325     330     335

```

RAW SEQUENCE LISTING ERROR SUMMARY
 PATENT APPLICATION: US/10/680,963

DATE: 12/21/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2
 Seq#:2; Xaa Pos. 2
 Seq#:5; N Pos. 9, 12, 18
 Seq#:6; N Pos. 6, 12
 Seq#:9; Xaa Pos. 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317
 Seq#:9; Xaa Pos. 318, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428
 Seq#:9; Xaa Pos. 429, 430, 431, 432, 433, 434, 435, 436
 Seq#:11; Xaa Pos. 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292
 Seq#:11; Xaa Pos. 293
 Seq#:25; Xaa Pos. 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222
 Seq#:25; Xaa Pos. 223, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246
 Seq#:27; Xaa Pos. 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196
 Seq#:27; Xaa Pos. 197, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220
 Seq#:29; Xaa Pos. 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189
 Seq#:29; Xaa Pos. 190, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213
 Seq#:31; Xaa Pos. 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189
 Seq#:31; Xaa Pos. 190, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213
 Seq#:75; N Pos. 17, 20

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1, 2, 3, 4, 5, 6, 41, 42, 47, 48, 49, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66
 Seq#:67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 94
 Seq#:95, 96, 97, 98, 99, 100, 101

VERIFICATION SUMMARY

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Input Set : A:\GFI-108 Sequence listing.ST25.txt

Output Set: N:\CRF4\12212004\J680963.raw

L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:168 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:176 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:288
M:341 Repeated in SeqNo=9
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:272
M:341 Repeated in SeqNo=11
L:1467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:208
M:341 Repeated in SeqNo=25
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:176
M:341 Repeated in SeqNo=27
L:1909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:160
M:341 Repeated in SeqNo=29
L:2126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:160
M:341 Repeated in SeqNo=31
L:2547 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:2555 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:3343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0